AMENDMENTS

IN THE CLAIMS

Please cancel claims 4 –20, 23 –30 and 33 –36, and add new claims 37 – 61, so that the claim set reads as follows:

1 – 36. (Canceled)

37. (New) A method for analyzing the sequence of a template comprising:

a) capturing the template with a sequencing reagent to form a captured template, said sequencing reagent being immobilized to a solid surface and comprising:

(i) a capture moiety capable of forming a stable duplex with a region of the template nucleic acid molecule;

(ii) a primer region comprising from 3 to 7 bases; and

between said capture moiety and said primer region

(iii) a spacer region that minimizes template independent noise; and

b) scanning the captured template using a primer-polymerase complex for regions of complementarity to the primer region and forming a duplex;

c) extending the primer region by at least one nucleotide moiety by means of a template-homology dependent extension reaction to form an extended primer; and

d) detecting the extended primer, wherein said detecting of the extended primer indicates the presence of one or more regions of complementarity to the primer region in the captured template;

wherein the steps of the method are repeated for an array of sequencing reagents so that a pattern of signals is generated for the template.

38. (New) The method of claim 37, wherein the solid surface is glass or plastic.

39. (New) The method of claim 37, wherein the solid surface is a glass plate, a quartz wafer, a nylon membrane, a nitrocellulose membrane, or a silicon wafer.

40. (New) The method of claim 37, wherein the solid surface is silicon glass.

41. (New) The method of claim 37, wherein the solid surface is polystyrene plastic.

42. (New) The method of claim 37, wherein the sequencing reagent further comprises an attachment moiety.

43. (New) The method of claim 42, wherein the sequence reagent has a 5'-terminus and the attachment moiety is located at or near said 5'-terminus.

44. (New) The method of claim 42, wherein the attachment moiety is an amino group, a thiol group, a disulfide group, or a biotin group.

45. (New) The method of claim 37, wherein the capture moiety comprises a sequence of 8-24 cytosine bases.

46. (New) The method of claim 37, wherein the capture moiety comprises a specific sequence complementary to a PCR primer or a portion thereof.

47. (New) The method of claim 37, wherein the spacer region is at least 10 nm in length.

48. (New) The method of claim 37, wherein the spacer region comprises a random, pseudo-random, or non-random sequence of nucleotide bases or analogs thereof.

49. (New) The method of claim 37, wherein the at least one nucleotide moiety is a non-chain terminating nucleotide or an analogue of a non-chain terminating nucleotide.

50. (New) The method of claim 49, wherein the at least one nucleotide moiety is a deoxynucleoside triphosphate base or ribonucleoside triphosphate base.

51. (New) The method of claim 37, wherein the at least one nucleotide moiety is a chain terminating nucleotide analogue.

52. (New) The method of claim 51, wherein the chain terminating nucleotide analogue is a dideoxynucleotide.

53. (New) The method of claim 37, wherein the at least one nucleotide moiety has a detectable labeled.

54. (New) The method of claim 53, wherein the detectable label is a fluorescent label.

55. (New) The method of claim 53, wherein the detectable label is a radioactive isotope.

56. (New) The method of claim 53, wherein the detectable label is an electron rich molecule.

57. (New) The method of claim 37, wherein the extended primer is detected by change in mass.

58. (New) The method of claim 37, wherein the density of sequence reagents in the array is at least 1000 elements/cm^2.

59. (New) The method of claim 57, wherein said change in mass is detected through mass spectrometry.

60. (New) The method of claim 37, wherein said primer region consists of from 4 to 6 bases.

61. (New) The method of claim 37, wherein the spacer is comprised of one or more of PNA sequences, glycol groups or 5'-nitroindole groups.